

IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/648,631

DATE: 10/08/2004 TIME: 15:32:28

Input Set : A:\66671-044.TXT

```
4 <110> APPLICANT: Hunter, Tony
        Kun Ping, Lu
7 <120> TITLE OF INVENTION: NIMA INTERACTING PROTEINS
10 <130> FILE REFERENCE: 66671-044
12 <140> CURRENT APPLICATION NUMBER: US 10/648,631
13 <141> CURRENT FILING DATE: 2003-08-25
15 <150> PRIOR APPLICATION NUMBER: US 10/616,410
16 <151> PRIOR FILING DATE: 2003-07-08
18 <160> NUMBER OF SEQ ID NOS: 22
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
                                                            110
23 <211> LENGTH: 1014
24 <212> TYPE: DNA
                                                              STANDARDED STANDARDE STANDARDE STANDARDE STANDARDE STANDARDE STANDARDE STANDARDE STANDARDE STANDARDE STANDARDE
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (25)...(513)
31 <400> SEQUENCE: 1
32 tgctggccag cacctcgagg gaag atg gcg gac gag gag aag ctg ccg ccc
                                                                              51
                                Met Ala Asp Glu Glu Lys Leu Pro Pro
33
36 ggc tgg gag aag cgc atg agc cgc agc tca ggc cga gtg tac tac ttc
                                                                              99
37 Gly Trp Glu Lys Arg Met Ser Arg Ser Ser Gly Arg Val Tyr Tyr Phe
                                               20
38 10
40 aac cac atc act aac gcc agc cag tgg gag cgg ccc agc ggc aac agc
                                                                             147
41 Asn His Ile Thr Asn Ala Ser Gln Trp Glu Arg Pro Ser Gly Asn Ser
                                           35
                      30
44 agc agt ggt ggc aaa aac ggg cag ggg gag cct gcc agg gtc cgc tgc
                                                                             195
 45 Ser Ser Gly Gly Lys Asn Gly Gln Gly Glu Pro Ala Arg Val Arg Cys
                  45
 48 tog cac ctg ctg gtg aag cac agc cag toa cgg cgg ccc tog toc tgg
                                                                              243
 49 Ser His Leu Leu Val Lys His Ser Gln Ser Arg Arg Pro Ser Ser Trp
                                   65
              60
 52 cgg cag gag aag atc acc cgg acc aag gag gag gcc ctg gag ctg atc
                                                                              291
 53 Arg Gln Glu Lys Ile Thr Arg Thr Lys Glu Glu Ala Leu Glu Leu Ile
                                                    85
                               80
 56 aac ggc tac atc cag aag atc aag tcg gga gag gac ttt gag tct
                                                                              339
 57 Asn Gly Tyr Ile Gln Lys Ile Lys Ser Gly Glu Glu Asp Phe Glu Ser
                                               100
 58 90
                                                                              387
 60 ctg gcc tca cag ttc agc gac tgc agc tca gcc aag gcc agg gga gac
 61 Leu Ala Ser Gln Phe Ser Asp Cys Ser Ser Ala Lys Ala Arg Gly Asp
                                           115
                     110
 64 ctg ggt gcc ttc agc aga ggt cag atg cag aag cca ttt gaa gac gcc
                                                                              435
```

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```
65 Leu Gly Ala Phe Ser Arg Gly Gln Met Gln Lys Pro Phe Glu Asp Ala
                                                       135
               125
68 tcg ttt gcg ctg cgg acg ggg gag atg agc ggg ccc gtg ttc acg gat
                                                                         483
69 Ser Phe Ala Leu Arg Thr Gly Glu Met Ser Gly Pro Val Phe Thr Asp
                               145
           140
72 tcc ggc atc cac atc atc ctc cgc act gag tgagggtggg gagcccaggc
                                                                         533
73 Ser Gly Ile His Ile Ile Leu Arg Thr Glu
76 etggeetegg ggeagggeag ggeggetagg eeggeeaget eeeeettgee egeeageeag
77 tggccgaacc ccccactccc tgccaccgtc acacagtatt tattgttccc acaatggctg
78 ggaggggcc cttccagatt ggggccctg gggtccccac tccctgtcca tccccagttg
                                                                         713
79 gggctgcgac cgccagattc tcccttaagg aattgacttc agcaggggtg ggaggctccc
                                                                         773
80 agacccaggg cagtgtggtg ggaggggtgt tccaaagaga aggcctggtc agcagagccg
                                                                         833
81 ccccgtgtcc ccccaggtgc tggaggcaga ctcgagggcc gaattgtttc tagttaggcc
82 acgeteetet gtteagtege aaaggtgaac acteatgegg cagecatggg ceetetgage
                                                                         953
83 aactgtgcag accetttcac ccccaattaa acccagaacc actaaaaaaa aaaaaaaaa
                                                                        1013
                                                                        1014
86 <210> SEQ ID NO: 2
87 <211> LENGTH: 163
88 <212> TYPE: PRT
89 <213 > ORGANISM: Homo sapiens
91 <400> SEQUENCE: 2
92 Met Ala Asp Glu Glu Lys Leu Pro Pro Gly Trp Glu Lys Arg Met Ser
93 1
94 Arg Ser Ser Gly Arg Val Tyr Tyr Phe Asn His Ile Thr Asn Ala Ser
               20
96 Gln Trp Glu Arg Pro Ser Gly Asn Ser Ser Ser Gly Gly Lys Asn Gly
                                40
98 Gln Gly Glu Pro Ala Arg Val Arg Cys Ser His Leu Leu Val Lys His
                            55
100 Ser Gln Ser Arg Arg Pro Ser Ser Trp Arg Gln Glu Lys Ile Thr Arg
                         70
102 Thr Lys Glu Glu Ala Leu Glu Leu Ile Asn Gly Tyr Ile Gln Lys Ile
                                         90
                     85
104 Lys Ser Gly Glu Glu Asp Phe Glu Ser Leu Ala Ser Gln Phe Ser Asp
                                     105
                 100
106 Cys Ser Ser Ala Lys Ala Arg Gly Asp Leu Gly Ala Phe Ser Arg Gly
                                                     125
                                 120
 107
             115
108 Gln Met Gln Lys Pro Phe Glu Asp Ala Ser Phe Ala Leu Arg Thr Gly
                             135
        130
110 Glu Met Ser Gly Pro Val Phe Thr Asp Ser Gly Ile His Ile Ile Leu
                                             155
                         150
 111 145
 112 Arg Thr Glu
 115 <210> SEQ ID NO: 3
 116 <211> LENGTH: 31
 117 <212> TYPE: DNA
 118 <213> ORGANISM: Homo sapiens
 120 <400> SEQUENCE: 3
                                                                        31
 121 gcgcctgcag tatctataya tggaataytg t
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123 <210> SEQ ID NO: 4
124 <211> LENGTH: 31
125 <212> TYPE: DNA
126 <213> ORGANISM: Homo sapiens
128 <400> SEQUENCE: 4
                                                                       31
129 gcgcggatcc rggtttcaga ggktyraasa g
131 <210> SEQ ID NO: 5
132 <211> LENGTH: 30
133 <212> TYPE: DNA
134 <213> ORGANISM: Homo sapiens
136 <400> SEQUENCE: 5
                                                                       30
137 gcgcgtacca agwccacygt ayattattcc
139 <210> SEQ ID NO: 6
140 <211> LENGTH: 13
141 <212> TYPE: PRT
142 <213> ORGANISM: Artificial Sequence
144 <220> FEATURE:
145 <223> OTHER INFORMATION: synthetic peptide
147 <400> SEQUENCE: 6
148 Met Tyr Asp Val Pro Asp Tyr Ala Ser Arg Pro Gln Asn
149 1
152 <210> SEQ ID NO: 7
153 <211> LENGTH: 32
154 <212> TYPE: PRT
155 <213> ORGANISM: Artificial Sequence
157 <220> FEATURE:
158 <223> OTHER INFORMATION: synthetic peptide
160 <400> SEQUENCE: 7
161 Met Ala Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Pro Glu Phe
162 1
                    5
163 Leu Val Asp Pro Pro Gly Ser Lys Asn Ser Ile Ala Arg Gly Lys Met
                                    25
167 <210> SEQ ID NO: 8
168 <211> LENGTH: 39
169 <212> TYPE: PRT
170 <213> ORGANISM: Homo sapiens
172 <400> SEQUENCE: 8
173 Glu Lys Leu Pro Pro Gly Trp Glu Lys Arg Met Ser Arg Ser Ser Gly
174 1
                     5
175 Arg Val Tyr Tyr Phe Asn His Ile Thr Asn Ala Ser Gln Trp Glu Arg
                                                         30
                                    25
176
                20
177 Pro Ser Gly Asn Ser Ser Ser
178
            35
181 <210> SEQ ID NO: 9
182 <211> LENGTH: 39
183 <212> TYPE: PRT
184 <213> ORGANISM: Yeast ESS1
186 <400> SEQUENCE: 9
187 Thr Gly Leu Pro Thr Pro Trp Thr Val Arg Tyr Ser Lys Ser Lys Lys
```

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```
188 1
                                         10
189 Arg Glu Tyr Phe Phe Asn Pro Glu Thr Lys His Ser Gln Trp Glu Glu
                                    25
                20
191 Pro Glu Gly Thr Asn Lys Asp
            35
195 <210> SEQ ID NO: 10
196 <211> LENGTH: 38
197 <212> TYPE: PRT
198 <213> ORGANISM: Homo sapiens
200 <400> SEQUENCE: 10
201 Val Pro Leu Pro Ala Gly Trp Glu Met Ala Lys Thr Ser Ser Gly Gln
203 Arg Tyr Phe Leu Asn His Ile Asp Gln Thr Thr Thr Trp Gln Asp Pro
                20
                                    25
205 Arg Lys Ala Met Leu Ser
206
            35
209 <210> SEQ ID NO: 11
210 <211> LENGTH: 38
211 <212> TYPE: PRT
212 <213 > ORGANISM: Mus musculus
214 <400> SEQUENCE: 11
215 Ser Pro Leu Pro Pro Gly Trp Glu Glu Arg Gln Asp Val Leu Gly Arg
                     5
217 Thr Tyr Tyr Val Asn His Glu Ser Arg Arg Thr Gln Trp Lys Arg Pro
                                                         30
               20
                                    25
219 Ser Pro Asp Asp Asp Leu
            35
223 <210> SEQ ID NO: 12
224 <211> LENGTH: 38
225 <212> TYPE: PRT
226 <213> ORGANISM: Yeast RSPS
228 <400> SEQUENCE: 12
229 Gly Arg Leu Pro Pro Gly Trp Glu Arg Arg Thr Asp Asn Phe Gly Arg
                     5
231 Thr Tyr Tyr Val Asp His Asn Thr Arg Thr Thr Thr Trp Lys Arg Pro
                20
                                    25
233 Thr Leu Asp Gln Thr Glu
            35
237 <210> SEQ ID NO: 13
238 <211> LENGTH: 38
239 <212> TYPE: PRT
240 <213 > ORGANISM: Homo sapiens
242 <400> SEQUENCE: 13
243 Thr Ser Val Gln Gly Pro Trp Glu Arg Ala Ile Ser Pro Asn Lys Val
244 1
                     5
                                         10
245 Pro Tyr Tyr Ile Asn His Glu Thr Gln Thr Thr Cys Trp Asp His Pro
247 Lys Met Thr Glu Leu Tyr
248
            35
```

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```
251 <210> SEQ ID NO: 14
252 <211> LENGTH: 37
253 <212> TYPE: PRT
254 <213> ORGANISM: Rattus rattus
256 <400> SEQUENCE: 14
257 Ser Asp Leu Pro Ala Gly Trp Met Arg Val Gln Asp Thr Ser Gly Thr
258 1
                    5
259 Tyr Tyr Trp His Ile Pro Thr Gly Thr Thr Gln Trp Glu Pro Pro Gly
    20
                                    25
261 Arg Ala Ser Pro Ser
           35
262
265 <210> SEQ ID NO: 15
266 <211> LENGTH: 14
267 <212> TYPE: PRT
268 <213> ORGANISM: Artificial Sequence
270 <220> FEATURE:
271 <223> OTHER INFORMATION: consensus sequence
273 <400> SEQUENCE: 15
274 Leu Pro Gly Trp Glu Gly Tyr Tyr Asn His Thr Thr Trp Pro
275 1
278 <210> SEQ ID NO: 16
279 <211> LENGTH: 105
280 <212> TYPE: PRT
281 <213> ORGANISM: Homo sapiens
283 <400> SEQUENCE: 16
284 His Leu Leu Val Lys His Ser Gln Ser Arg Arg Pro Ser Ser Trp Arg
286 Gln Glu Lys Ile Thr Arg Thr Lys Glu Glu Ala Leu Glu Leu Ile Asn
288 Gly Tyr Ile Gln Lys Ile Lys Ser Gly Glu Glu Asp Phe Glu Ser Leu
                                40
290 Ala Ser Gln Phe Ser Asp Cys Ser Ser Ala Lys Ala Arg Gly Asp Leu
                           55
292 Gly Ala Phe Ser Arg Gly Gln Met Gln Lys Pro Phe Glu Asp Ala Ser
                        70
294 Phe Ala Leu Arg Thr Gly Glu Met Ser Gly Pro Val Phe Thr Asp Ser
                    85
296 Gly Ile His Ile Ile Leu Arg Thr Glu
297
300 <210> SEQ ID NO: 17
301 <211> LENGTH: 107
302 <212> TYPE: PRT
303 <213> ORGANISM: Yeast ESS1
305 <400> SEQUENCE: 17
306 His Ile Leu Ile Lys His Lys Asp Ser Arg Arg Pro Ala Ser His Arg
                     5
308 Ser Glu Asn Ile Thr Ile Ser Lys Gln Asp Ala Thr Asp Glu Leu Lys
                                    25
        20
310 Thr Leu Ile Thr Arg Leu Asp Asp Ser Lys Thr Asn Ser Phe Glu
```

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